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SEQUENCE LISTING

<110> Wright, David A.
Voytas, Daniel F.

<120> PLANT RETROELEMENTS AND METHODS RELATED THERETO

<130> 08411-030002

<140> 09/965,553
<141> 2001-09-27

<150> 09/322,478
<151> 1999-05-28

<150> 60/087,125
<151> 1998-05-29

<160> 62

<170> FastSEQ for Windows Version 4.0

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<400> 4

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1 5

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atccttccag agaggaatgt agagcttgga ccagggatgt ttgatgagtt cctgcaggaa 180
ctccagaggc tcagatggga ccaggttctg acccgacttc cagagaagtg gattgatgtt 240
gctctggtga aggagtttta ctccaaccta tatgatccag aggaccacag tccgaagttt 300
tggagtgttc gaggacaggt tgtgagattt gatgctgaga cgattaatga tttcctcgac 360
accccggtca tcttggcaga gggagaggat tatccagcct actctcagta cctcagcact 420
cctccagacc atgatgccat cctttccgct ctgtgtactc caggggacg atttgttctg 480
aatgttgata gtgccccctg gaagctgctg cggaaggatc tgatgacgct cgcgcagaca 540
tggagtgtgc tctcttattt taaccttgca ctgacttttc acacttctga tattaatgtt 600
gacagggccc gactcaatta tggcttggtg atgaagatgg acctggacgt gggcagcctc 660
atttctcttc agatcagtca gatcgcccag tccatcactt ccaggcttgg gttcccagcg 720
ttgatcacaa cactgtgtga gattcagggg gttgtctctg ataccctgat ttttgagtca 780
ctcagtcctg tgatcaacct tgcctacatt aagaagaact gctggaaccc tgccgatcca 840
tctatcacat ttcaggggac ccgccgcacg cgcaccagag cttcggcgtc ggcatctgag 900
gctcctcttc catcccagca tccttctcag ccttttccc agagaccacg gcctccactt 960
ctatccacct cagcacctcc atacatgcat ggacagatgc tcaggtcctt gtaccagggt 1020
cagcagatca tcattcagaa cctgtatcga ttgtccctac atttgcagat ggatctgcca 1080
ctcatgactc cggaggccta tcgtcagcag gtcgccaagc taggagacca gccctccact 1140
gacaggggg aagagccttc tggagccgct gctactgagg atcctgccgt tgatgaagac 1200
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<212> PRT
<213> Artificial Sequence

<220>
<223> plant retroelement sequence

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Asn Trp Asp Ser Ser Arg Phe Thr Phe Glu Ile Ala Trp His Arg Tyr
20 25 30
Gln Asp Ser Ile Gln Leu Arg Asn Ile Leu Pro Glu Arg Asn Val Glu
35 40 45
Leu Gly Pro Gly Met Phe Asp Glu Phe Leu Gln Glu Leu Gln Arg Leu
50 55 60
Arg Trp Asp Gln Val Leu Thr Arg Leu Pro Glu Lys Trp Ile Asp Val
65 70 75 80
Ala Leu Val Lys Glu Phe Tyr Ser Asn Leu Tyr Asp Pro Glu Asp His
85 90 95
Ser Pro Lys Phe Trp Ser Val Arg Gly Gln Val Val Arg Phe Asp Ala

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            100                 105                 110
Glu Thr Ile Asn Asp Phe Leu Asp Thr Pro Val Ile Leu Ala Glu Gly
        115                 120                 125
Glu Asp Tyr Pro Ala Tyr Ser Gln Tyr Leu Ser Thr Pro Pro Asp His
    130                 135                 140
Asp Ala Ile Leu Ser Ala Leu Cys Thr Pro Gly Gly Arg Phe Val Leu
145                 150                 155                 160
Asn Val Asp Ser Ala Pro Trp Lys Leu Leu Arg Lys Asp Leu Met Thr
                165                 170                 175
Leu Ala Gln Thr Trp Ser Val Leu Ser Tyr Phe Asn Leu Ala Leu Thr
            180                 185                 190
Phe His Thr Ser Asp Ile Asn Val Asp Arg Ala Arg Leu Asn Tyr Gly
        195                 200                 205
Leu Val Met Lys Met Asp Leu Asp Val Gly Ser Leu Ile Ser Leu Gln
    210                 215                 220
Ile Ser Gln Ile Ala Gln Ser Ile Thr Ser Arg Leu Gly Phe Pro Ala
225                 230                 235                 240
Leu Ile Thr Thr Leu Cys Glu Ile Gln Gly Val Val Ser Asp Thr Leu
                245                 250                 255
Ile Phe Glu Ser Leu Ser Pro Val Ile Asn Leu Ala Tyr Ile Lys Lys
            260                 265                 270
Asn Cys Trp Asn Pro Ala Asp Pro Ser Ile Thr Phe Gln Gly Thr Arg
        275                 280                 285
Arg Thr Arg Thr Arg Ala Ser Ala Ser Ala Ser Glu Ala Pro Leu Pro
    290                 295                 300
Ser Gln His Pro Ser Gln Pro Phe Ser Gln Arg Pro Arg Pro Pro Leu
305                 310                 315                 320
Leu Ser Thr Ser Ala Pro Pro Tyr Met His Gly Gln Met Leu Arg Ser
                325                 330                 335
Leu Tyr Gln Gly Gln Gln Ile Ile Ile Gln Asn Leu Tyr Arg Leu Ser
            340                 345                 350
Leu His Leu Gln Met Asp Leu Pro Leu Met Thr Pro Glu Ala Tyr Arg
        355                 360                 365
Gln Gln Val Ala Lys Leu Gly Asp Gln Pro Ser Thr Asp Arg Gly Glu
    370                 375                 380
Glu Pro Ser Gly Ala Ala Ala Thr Glu Asp Pro Ala Val Asp Glu Asp
385                 390                 395                 400
Leu Ile Ala Asp Leu Ala Gly Ala Asp Trp Ser Pro Trp Ala Asp Leu
                405                 410                 415
Gly Arg Gly Ser Glx
            420
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<210> 7
<211> 1596
<212> DNA
<213> Artificial Sequence

<220>
<223> plant retroelement sequence

<400> 7

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tgtcggcgta acaacgctgc aagaagaaga agggagcaag acatagaagg aagtagttac     120
acctcacctc ctccttctcc aaattatgct cagatggacg gggaaccggc acaaagagtc     180
acactagagg acttctctaa taccaccact cctcagttct ttacaagtat cacaaggccg     240
gaagtccaag cagatctcct tactcaaggg aacctcttcc atggtcttcc aaatgaagat     300
ccatatgcgc atctagcctc atacatagag atatgcagca ccgttaaaat cgccggagtt     360
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ccaaaagatg cgatactcct taacctcttt tccttttccc tagcaggaga ggcaaaaaga     420
tggttgcact cctttaaagg caatagctta agaacatggg aagaagtagt ggaaaaattc     480
ttaaagaagt atttcccaga gtcaaagacc gtcgaacgaa agatggagat ttcttatttc     540
catcaatttc tggatgaatc ccttagcgaa gcactagacc atttccacgg attgctaaga     600
aaaacaccaa cacacagata cagcgagcca gtacaactaa acatattcat cgatgacttg     660
caactcttaa tcgaaacagc tactagaggg aagatcaagc tgaagactcc cgaagaagcg     720
atggagctcg tcgagaacat ggcggctagc gatcaagcaa tccttcatga tcacacttat     780
gttcccacaa aaagaagcct cttggagctt agcacgcagg acgcaacttt ggtacaaaac     840
aagctgttga cgaggcagat agaagccctc atcgaaaccc tcagcaagct gcctcaacaa     900
ttacaagcga taagttcttc ccactcttct gttttgcagg tagaagaatg ccccacatgc     960
agagggacac atgagcctgg acaatgtgca agccaacaag acccctctcg tgaagtaaat    1020
tatataggca tactaaatcg ttacggattt cagggctaca accagggaaa tccatctgga    1080
ttcaatcaag gggcaacaag atttaatcac gagccaccgg ggtttaatca aggaagaaac    1140
ttcatgcaag gctcaagttg gacgaataaa ggaaatcaat ataaggagca aaggaaccaa    1200
ccaccatacc agccaccata ccagcaccct agccaaggtc cgaatcagca agaaaagccc    1260
accaaaatag aggaactgct gctgcaattc atcaaggaga caagatcaca tcaaaagagc    1320
acggatgcag ccattcggaa tctagaagtt caaatgggcc aactggcgca tgacaaagcc    1380
gaacggccca ctagaacttt cggtgctaac atggagagaa gaaccccaag gaaggataaa    1440
gcagtactga ctagagggca gagaagagcg caggaggagg gtaaggttga aggagaagac    1500
tggccagaag aaggaaggac agagaagaca gaagaagaag agaaggtggc agaagaacct    1560
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<210> 8
<211> 532
<212> PRT
<213> Artificial Sequence

<220>
<223> plant retroelement sequence

<400> 8

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Met Arg Gly Arg Thr Ala Ser Gly Asp Val Val Pro Ile Asn Leu Glu
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Ile Glu Ala Thr Cys Arg Arg Asn Asn Ala Ala Arg Arg Arg Arg Glu
            20                  25                  30
Gln Asp Ile Glu Gly Ser Ser Tyr Thr Ser Pro Pro Pro Ser Pro Asn
        35                  40                  45
Tyr Ala Gln Met Asp Gly Glu Pro Ala Gln Arg Val Thr Leu Glu Asp
    50                  55                  60
Phe Ser Asn Thr Thr Thr Pro Gln Phe Phe Thr Ser Ile Thr Arg Pro
65                  70                  75                  80
Glu Val Gln Ala Asp Leu Leu Thr Gln Gly Asn Leu Phe His Gly Leu
                85                  90                  95
Pro Asn Glu Asp Pro Tyr Ala His Leu Ala Ser Tyr Ile Glu Ile Cys
            100                 105                 110
Ser Thr Val Lys Ile Ala Gly Val Pro Lys Asp Ala Ile Leu Leu Asn
        115                 120                 125
Leu Phe Ser Phe Ser Leu Ala Gly Glu Ala Lys Arg Trp Leu His Ser
    130                 135                 140
Phe Lys Gly Asn Ser Leu Arg Thr Trp Glu Glu Val Val Glu Lys Phe
145                 150                 155                 160
Leu Lys Lys Tyr Phe Pro Glu Ser Lys Thr Val Glu Arg Lys Met Glu
                165                 170                 175
Ile Ser Tyr Phe His Gln Phe Leu Asp Glu Ser Leu Ser Glu Ala Leu
            180                 185                 190
Asp His Phe His Gly Leu Leu Arg Lys Thr Pro Thr His Arg Tyr Ser
        195                 200                 205
```

```
Glu Pro Val Gln Leu Asn Ile Phe Ile Asp Asp Leu Gln Leu Leu Ile
    210                 215                 220
Glu Thr Ala Thr Arg Gly Lys Ile Lys Leu Lys Thr Pro Glu Glu Ala
225                 230                 235                 240
Met Glu Leu Val Glu Asn Met Ala Ala Ser Asp Gln Ala Ile Leu His
                245                 250                 255
Asp His Thr Tyr Val Pro Thr Lys Arg Ser Leu Leu Glu Leu Ser Thr
            260                 265                 270
Gln Asp Ala Thr Leu Val Gln Asn Lys Leu Leu Thr Arg Gln Ile Glu
        275                 280                 285
Ala Leu Ile Glu Thr Leu Ser Lys Leu Pro Gln Gln Leu Gln Ala Ile
    290                 295                 300
Ser Ser Ser His Ser Ser Val Leu Gln Val Glu Glu Cys Pro Thr Cys
305                 310                 315                 320
Arg Gly Thr His Glu Pro Gly Gln Cys Ala Ser Gln Gln Asp Pro Ser
                325                 330                 335
Arg Glu Val Asn Tyr Ile Gly Ile Leu Asn Arg Tyr Gly Phe Gln Gly
            340                 345                 350
Tyr Asn Gln Gly Asn Pro Ser Gly Phe Asn Gln Gly Ala Thr Arg Phe
        355                 360                 365
Asn His Glu Pro Pro Gly Phe Asn Gln Gly Arg Asn Phe Met Gln Gly
    370                 375                 380
Ser Ser Trp Thr Asn Lys Gly Asn Gln Tyr Lys Glu Gln Arg Asn Gln
385                 390                 395                 400
Pro Pro Tyr Gln Pro Pro Tyr Gln His Pro Ser Gln Gly Pro Asn Gln
                405                 410                 415
Gln Glu Lys Pro Thr Lys Ile Glu Glu Leu Leu Leu Gln Phe Ile Lys
            420                 425                 430
Glu Thr Arg Ser His Gln Lys Ser Thr Asp Ala Ala Ile Arg Asn Leu
        435                 440                 445
Glu Val Gln Met Gly Gln Leu Ala His Asp Lys Ala Glu Arg Pro Thr
    450                 455                 460
Arg Thr Phe Gly Ala Asn Met Glu Arg Arg Thr Pro Arg Lys Asp Lys
465                 470                 475                 480
Ala Val Leu Thr Arg Gly Gln Arg Arg Ala Gln Glu Glu Gly Lys Val
                485                 490                 495
Glu Gly Glu Asp Trp Pro Glu Glu Gly Arg Thr Glu Lys Thr Glu Glu
            500                 505                 510
Glu Glu Lys Val Ala Glu Glu Pro Lys Arg Thr Lys Ser Gln Arg Ala
        515                 520                 525
Arg Glu Ala Lys
    530
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<211> 603
<212> DNA
<213> Artificial Sequence

<220>
<223> plant retroelement sequence

<400> 9

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atcatggaag tagagatctt tgactgttgg ggcatagact tcatggggcc ttttccttcg     120
tcatacggga atgtctacat cttggtagct gtggattacg tctccaaatg ggtggaagcc     180
atagccacgc caaaggacga tgccagggta gtgatcaaat ttctgaagaa gaacattttt     240
tcccgttttg gagtcccacg agccttgatt agtgataggg gaacgcactt ctgcaacaat     300
```

cagttgaaga aagtcctgga gcactataat gtccgacata aggtggccac accttatcac 360
cctcagacaa atggccaagc agaaatttct aacagggagc tcaagcgaat cctggaaaag 420
acagttgcat caacaagaaa ggattggtcc ttgaagctcg atgatgctct ctgggcctat 480
aggacagcgt tcaagactcc catcggctta tcaccatttc agctagtgta tgggaaggca 540
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gac 603

<210> 10
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> plant retroelement sequence

<400> 10
Cys Asp Lys Cys Gln Arg Thr Gly Gly Ile Ser Arg Arg Asn Glu Met
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Pro Leu Gln Asn Ile Met Glu Val Glu Ile Phe Asp Cys Trp Gly Ile
20 25 30
Asp Phe Met Gly Pro Phe Pro Ser Ser Tyr Gly Asn Val Tyr Ile Leu
35 40 45
Val Ala Val Asp Tyr Val Ser Lys Trp Val Glu Ala Ile Ala Thr Pro
50 55 60
Lys Asp Asp Ala Arg Val Val Ile Lys Phe Leu Lys Lys Asn Ile Phe
65 70 75 80
Ser Arg Phe Gly Val Pro Arg Ala Leu Ile Ser Asp Arg Gly Thr His
85 90 95
Phe Cys Asn Asn Gln Leu Lys Lys Val Leu Glu His Tyr Asn Val Arg
100 105 110
His Lys Val Ala Thr Pro Tyr His Pro Gln Thr Asn Gly Gln Ala Glu
115 120 125
Ile Ser Asn Arg Glu Leu Lys Arg Ile Leu Glu Lys Thr Val Ala Ser
130 135 140
Thr Arg Lys Asp Trp Ser Leu Lys Leu Asp Asp Ala Leu Trp Ala Tyr
145 150 155 160
Arg Thr Ala Phe Lys Thr Pro Ile Gly Leu Ser Pro Phe Gln Leu Val
165 170 175
Tyr Gly Lys Ala Cys His Leu Pro Val Glu Leu Glu Tyr Lys Ala Tyr
180 185 190
Trp Ala Leu Lys Leu Leu Asn Phe Asp
195 200

<210> 11
<211> 600
<212> DNA
<213> Artificial Sequence

<220>
<223> plant retroelement sequence

<400> 11
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aaggaccatt tccccttacc tttcatggat cagatgctgg agagacttgc agggcaggca 240
tactactgtt tcttggatgg atactcggga tacaaccaga tcgcggtaga ccccagagat 300

caggagaaga cggcctttac atgccccttt ggcgtctttg cttacagaag gatgccattc 360
gggttatgta atgcaccagc cacatttcag aggtgcatgc tggccatttt ttcagacatg 420
gtggagaaaa gcatcgaggt atttatggac gacttctcgg tttttggacc ctcatttgac 480
agctgtttga ggaacctaga gagggtactt cagaggtgcg aagagactaa cttggtactg 540
aattgggaaa agtgtcattt catggttcga gagggcatag tcctaggcca caagatctca 600

<210> 12
<211> 200
<212> PRT
<213> Artificial Sequence

<220>
<223> plant retroelement sequence

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 1   5   10   15
Pro Val Gln Val Val Pro Lys Lys Gly Gly Met Thr Val Val Arg Asp
            20   25   30
Glu Arg Asn Asp Leu Ile Pro Thr Arg Thr Val Thr Gly Trp Arg Met
        35   40   45
Cys Ile Asp Tyr Arg Lys Leu Asn Glu Ala Thr Arg Lys Asp His Phe
    50   55   60
Pro Leu Pro Phe Met Asp Gln Met Leu Glu Arg Leu Ala Gly Gln Ala
65   70   75   80
Tyr Tyr Cys Phe Leu Asp Gly Tyr Ser Gly Tyr Asn Gln Ile Ala Val
                85   90   95
Asp Pro Arg Asp Gln Glu Lys Thr Ala Phe Thr Cys Pro Phe Gly Val
            100   105   110
Phe Ala Tyr Arg Arg Met Pro Phe Gly Leu Cys Asn Ala Pro Ala Thr
        115   120   125
Phe Gln Arg Cys Met Leu Ala Ile Phe Ser Asp Met Val Glu Lys Ser
    130   135   140
Ile Glu Val Phe Met Asp Asp Phe Ser Val Phe Gly Pro Ser Phe Asp
145   150   155   160
Ser Cys Leu Arg Asn Leu Glu Arg Val Leu Gln Arg Cys Glu Glu Thr
                165   170   175
Asn Leu Val Leu Asn Trp Glu Lys Cys His Phe Met Val Arg Glu Gly
            180   185   190
Ile Val Leu Gly His Lys Ile Ser
        195   200

<210> 13
<211> 858
<212> DNA
<213> Artificial Sequence

<220>
<223> plant retroelement sequence

<400> 13
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ccattcgggg aagccttaca gcagatgccc ctctactcca aatttatgaa agacatcctc 180
accaagaagg ggaagtatat tgacaacgag aatattgtgg taggaggcaa ttgcagtgcg 240
ataatacaaa ggattctacc caagaagttt aaagaccccg gaagtgttac catcccgtgc 300
accattggga aggaagccgt aaacaaggcc ctcattgatc taggagcaag tatcaatctg 360

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atgcccttgt caatgtgcaa aagaattggg aatttgaaga tagatcccac caagatgacg     420
cttcaactgg cagaccgctc aatcacaagg ccatatgggg tggtagaaga tgtcctggtc     480
aaggtacgcc acttcacttt tccggtggac tttgttatca tggatatcga agaagacact     540
gagattcccc ttatcttagg cagacccttc atgctgactg ccaactgtgt ggtggatatg     600
gggaaaggga acttagagtt gactattgat aatcagaaga tcacctttga ccttatcaag     660
gcaatgaagt acccacagga gggttggaag tgcttcagaa tagaggagat tgatgaggaa     720
gatgtcagtt ttctcgagac accaaagact tcgctagaaa aagcaatggt aaatcattta     780
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gaagacagta ttcctgag                                                  858
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<210> 14
<211> 286
<212> PRT
<213> Artificial Sequence

<220>
<223> plant retroelement sequence

<400> 14

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Pro Thr Lys Lys Asn Lys Glu Arg Tyr Phe Ala Arg Phe Leu Glu Ile
            20                  25                  30
Phe Lys Gly Leu Glu Ile Thr Met Pro Phe Gly Glu Ala Leu Gln Gln
        35                  40                  45
Met Pro Leu Tyr Ser Lys Phe Met Lys Asp Ile Leu Thr Lys Lys Gly
    50                  55                  60
Lys Tyr Ile Asp Asn Glu Asn Ile Val Val Gly Gly Asn Cys Ser Ala
65                  70                  75                  80
Ile Ile Gln Arg Ile Leu Pro Lys Lys Phe Lys Asp Pro Gly Ser Val
                85                  90                  95
Thr Ile Pro Cys Thr Ile Gly Lys Glu Ala Val Asn Lys Ala Leu Ile
            100                 105                 110
Asp Leu Gly Ala Ser Ile Asn Leu Met Pro Leu Ser Met Cys Lys Arg
        115                 120                 125
Ile Gly Asn Leu Lys Ile Asp Pro Thr Lys Met Thr Leu Gln Leu Ala
    130                 135                 140
Asp Arg Ser Ile Thr Arg Pro Tyr Gly Val Val Glu Asp Val Leu Val
145                 150                 155                 160
Lys Val Arg His Phe Thr Phe Pro Val Asp Phe Val Ile Met Asp Ile
                165                 170                 175
Glu Glu Asp Thr Glu Ile Pro Leu Ile Leu Gly Arg Pro Phe Met Leu
            180                 185                 190
Thr Ala Asn Cys Val Val Asp Met Gly Lys Gly Asn Leu Glu Leu Thr
        195                 200                 205
Ile Asp Asn Gln Lys Ile Thr Phe Asp Leu Ile Lys Ala Met Lys Tyr
    210                 215                 220
Pro Gln Glu Gly Trp Lys Cys Phe Arg Ile Glu Glu Ile Asp Glu Glu
225                 230                 235                 240
Asp Val Ser Phe Leu Glu Thr Pro Lys Thr Ser Leu Glu Lys Ala Met
                245                 250                 255
Val Asn His Leu Asp Cys Leu Thr Ser Glu Glu Glu Glu Asp Leu Lys
            260                 265                 270
Ala Cys Leu Glu Asn Leu Asp Gln Glu Asp Ser Ile Pro Glu
        275                 280                 285
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<210> 15

<211> 192
<212> DNA
<213> Artificial Sequence

<220>
<223> plant retroelement sequence

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tatgcaacca cagaaaagga gatgctagcc attgtctttg ccttggagaa gttcaggtca 180
tacttgatag gg 192

<210> 16
<211> 64
<212> PRT
<213> Artificial Sequence

<220>
<223> plant retroelement sequence

<400> 16
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1 5 10 15
Gly Gln Arg Lys Asp Lys Val Phe His Ala Ile Tyr Tyr Ala Ser Lys
20 25 30
Val Leu Asn Glu Ala Gln Leu Asn Tyr Ala Thr Thr Glu Lys Glu Met
35 40 45
Leu Ala Ile Val Phe Ala Leu Glu Lys Phe Arg Ser Tyr Leu Ile Gly
50 55 60

<210> 17
<211> 12286
<212> DNA
<213> Artificial Sequence

<220>
<223> plant retroelement sequence

<400> 17
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gccatagata tgaaaactga aggtacaaca agcaaaaggc agcagaaagt gaagaaaaag 180
aataaaatct gaagcagacc cagcccaaca cgcgccctta gcgcgcgtca cgcgctaagc 240
ttgcaaggca gcacaggcac taagcgaggc gttaagcacg aagatgcagg attcgttacg 300
tgcgctaagc gcgaggcaca cgctaagcgc gcgatccaac agaagcacac gctaagcctg 360
cagcatgcgc taagcgcgcc tacgaaggcc caaagcccat ttctacacct ataaatagag 420
atccaagcca agggagaatg tacaccttgc ctcagagcac ttctctcagc attccaagct 480
tgagctctcc cttttctctc tatattcttt gcttttatta tccattcttt ctttcacccc 540
agttgtaaag cccctcaatg gccatgagtg gttaatcccc tagctacggc ctggtaggcc 600
taaaaagcca atgatgtatg gtgtacttca agagttatca atgcaaagag gattcattcc 660
aggttttatg ttctaattct ttccttttta tcttgcattt atgtcttaaa tttctgttgg 720
gttttattcg ctcgggagag ggtatttcct aataagggtt taagaagtaa tgcatgcatc 780
agttttaggg gttatacgct tggtaaaggg taacacctaa tagaacaaat taagaaaagg 840
atcgtcgggc tagcattgct aggcatagaa tgatggccca atgcccatgc atttagcaac 900
atctagaatt taaccttaat gcatttaat tattgaatct tcacaaaggc atttgggaga 960
taggtagtta aaataggctt gtcatcgtga ggcatcaagg gcaagtaaaa ttaatagatg 1020

tgggtagaac taattcaact gcattggtaa tgaacatcat aaattcattc atcgtaggcc 1080
aattaggttt gtccggtctt ggcattttca tcaattgtct tcctaaatta tttgatctaa 1140
tagcaacaat ttattcttat gcctattcct gtttttacta tttactttta cttacaaatt 1200
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Phe Ser Asn Thr Thr Thr Pro Gln Phe Phe Thr Ser Ile Thr Arg Pro
65                  70                  75                  80
Glu Val Gln Ala Asp Leu Leu Thr Gln Gly Asn Leu Phe His Gly Leu
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Pro Asn Glu Asp Pro Tyr Ala His Leu Ala Ser Tyr Ile Glu Ile Cys
            100                 105                 110
Ser Thr Val Lys Ile Ala Gly Val Pro Lys Asp Ala Ile Leu Leu Asn
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Ile Ser Tyr Phe His Gln Phe Leu Asp Glu Ser Leu Ser Glu Ala Leu
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Asp His Phe His Gly Leu Leu Arg Lys Thr Pro Thr His Arg Tyr Ser
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ttggatgcga gaatgattta cccgatctcg gatagtccat gggtcagtcc cgtgcatgtg 60
gttccgaaga aaggtggaaa taccgtcatc cggaatgaca aggatgaatt gatccctacc 120
aaagttgcaa cggggtggag aatgtgtatt gaatataggc ggttgaatac cgcaactcga 180
aaggaccatt ttccactccc gttcatggat caaatgctgg aaagactctc cgggcaacaa 240
tactattgtt tcttggatgg ctattccggg tataaccaaa ttgccgttga cccggccgat 300
cattaaaaga cggctttcac atgtccgttt ggagtgttcg cataccgaaa aatgtccttt 360
gggttgtgca atgcaccgac gactttccaa cgatgtgtgc aagccatttt tgccgacctt 420
aatgagaaaa caatggaagt cttcatggat gacttctcgg tatttggtgt atcctttagt 480
ttatgcttgg caaacttgaa aacggtgctt gaaagatgtg tgaagaccaa tcttgtgctt 540

aattggtaga agtgccactt catggtgacc gaggggatag tgcttggcca taaagtc 597

<210> 30
<211> 192
<212> DNA
<213> Pisum sativum

<400> 30
tttgagctaa tgtgtgatgc gagcaactat gcaatcggag cggtattagg ccaaagaaaa 60
gagaaaaaat ttcatgcgat acattacgca agtaaagttc ttaatgaggc tcaaattaac 120
tatgccacca ctgaaaaaga attacttgcg atagtgtatg cacttgaaaa gtttaggtct 180
tatcttatag gg 192

<210> 31
<211> 581
<212> DNA
<213> Pisum sativum

<400> 31
tgtgatagtt gccagagaag cggtgggatt ggtaagagag acgagatgtc tctccaaaac 60
atccaagagg tcgaagtatt tgattgttgg ggcatcgatt ttgtaggacc attccccccc 120
cttatggtaa cgagtatatg cttgtcgcag ttgaggcgat tgcctcacct cgggcggatg 180
cgaaaacggt aataattttt ttgaagaaaa acatattttc ccgtttcgga acccccccgag 240
tgttgataag tgacggaggg tcacactttt gtaatgcacc gttggaaagc attttaaaac 300
attacggtgt atcacacaga gtggcaactc cgtatcaccc acaggctaat ggacaagccg 360
aggtctctaa tcgtgagatt aagagaattc tcgaaaaaac tgtgtcaaat tcgaaaaaag 420
agtggtcaca aaaattggat gaagcgttat gggcataccg taccgccttt aaagctccaa 480
ttgggctcac tccttttcaa ttggtgtttg gtaaaacttg ccatttgccg gtcgaattgg 540
agcacaaagc cttgtgggct ttgaaaatta ataattttga a 581

<210> 32
<211> 1362
<212> DNA
<213> Glycine max

<400> 32
atggcctcct gtaaacaccg agctgtgccc acacccgggg aagcgtccaa ctgggactct 60
tcacgtttca ctttcgagat tgcttggcac agataccagg atagcattca gctccggaac 120
atccttccag agaggaatgt agagcttgga ccagggatgt ttgatgagtt cctgcaggaa 180
ctccagaggc tcagatggga ccaggttctg acccgacttc cagagaagtg gattgatgtt 240
gctctggtga aggagtttta ctccaaccta tatgatccag aggaccacag tccgaagttt 300
tggagtgttc gaggacaggt tgtgagattt gatgctgaga cgattaatga tttcctcgac 360
accccggtca tcttggcaga gggagaggat tatccagcct actctcagta cctcagcact 420
cctccagacc atgatgccat cctttccgct ctgtgtactc caggggacg atttgttctg 480
aatgttgata gtgccccctg gaagctgctg cggaaggatc tgatgacgct cgcgcagaca 540
tggagtgtgc tctcttattt taaccttgca ctgacttttc acacttctga tattaatgtt 600
gacagggccc gactcaatta tggcttggtg atgaagatgg acctggacgt gggcagcctc 660
atttctcttt agatcagtca gatcgcccag tccatcactt ccaggcttgg gttcccagcg 720
ttgatcacaa cactgtgtga gattcagggg gttgtctctg ataccctgat ttttgagtca 780
ctcagtcctg tgatcaacct tgcctacatt aagaagaact gctggaaccc tgccgatcca 840
tctatcacat ttcaggggac ccgccgcacg cgcaccagag cttcggcgtc ggcatctgag 900
gctcctcttc catcccagca tccttctcag ccttttccc agtgaccacg gcctccactt 960
ctatccacct cagcacctcc atacatgcat ggacagatgc tcaggtcctt gtaccagggt 1020
cagcagatca tcattcagaa cctgtatcga ttgtccctac atttgcagat ggatctgcca 1080
ctcatgactc cggaggccta tcgtcagcag gtcgcctagc taggagacca gccctccact 1140
gacaggggg aagagccttc tggagccgct gctactgagg atcctgccgt tgatgaagac 1200
ctcatagctg acttggctgg cgctgattgg agcccatggg cagacttggg cagaggcagc 1260

tgatcttatg ctttaatgtt ttcttttata ttatgtttgt gttctctttt atgttttatg 1320
ttatgttttt atgtagtctg tttggtaatt aaaaagaggt ag 1362

<210> 33
<211> 192
<212> DNA
<213> Glycine max

<400> 33
tttgagttga tgtgtgacgc gagcgattat gctataggtg cagtgcttgg acaaaggaag 60
ggcaaaattt ttcatgctat ctactacgcc agcaaagttt taaatgatgc acaggttaac 120
tatgctacca cagaaaaaga aatgttggca attgtttatg cacttgaaaa gttcaaatct 180
tatttggtag gc 192

<210> 34
<211> 597
<212> DNA
<213> Glycine max

<400> 34
ttggaggttg ggctcatata ccccatctct gacaacgctt gggtaagccc agtacaggtg 60
gttcccaaga aaggtggaat gacagtggta caaaatgaga ggaatgactt gataccaaca 120
cgaacagtca ctggctggcg aatgtgtatt gactatcaca agctgaatga agctacacgg 180
aaggaccatt tccccttacc tttcatggat cagatgctgg agagacttgc agggcaggca 240
tactactgtt tcttggatgg atactcggga tacaaccaga tcgcggtaga ccccatagat 300
caggagaaga cggtctttac atgccccttt ggcgtctttg cttacagaag gatgtcattc 360
gggttatgta atgtaccagc cacatttcag aggtgcatgc tgaccatttt ttcagacatg 420
gtggagaaaa gcatcgaggt atttatggac gacttctcgg tttttggacc ctcatttgac 480
agctgtttga ggaacctaga aatggtactt cagaggtgcg tagagactaa cttggtactg 540
aattgggaaa agtgtcattt tatggttcga gagggcatag tcctaggcca caagatc 597

<210> 35
<211> 603
<212> DNA
<213> Glycine max

<400> 35
tgtgataaat gtcagagaac aaggggggata tctcgaagaa atgagatgcc tttgcagaat 60
atcatggagg tagagatctt tgatagttgg ggcatagact tcatggggcc tcttccttca 120
tcatacagga atgtctacat cttggtagct gtggattacg tctccaaatg ggtggaagcc 180
atagccacgc tgaaggacga tgccagggta gtgatcaaat ttctgaagaa gaacattttt 240
tcccatttcg gagtcccacg agccttgatt agtgatgggg gaacgcactt ctgcaacaat 300
cagttgaaga aagtcctgga gcactataat gtccgacaca aggtggccac accttatcac 360
actcagacga atggccaagc agaaatttct aacagggagc tcaagcgaat cctggaaaag 420
acagttgcat catcaagaaa ggattgggcc ttgaagctcg atgatactct ctgggcctat 480
aggacagcgt tcaagactcc catcggctta tcaccatttc agctagtata tgggaaggca 540
tgtcatttac cagtagagct ggagcacaag gcatattggg ctctcaagtt gctcaacttt 600
gac 603

<210> 36
<211> 150
<212> DNA
<213> Glycine max

<400> 36
cctaaaatac tacaacgaca tgattggtgt tttaggataa ttgactgaaa aacctattat 60
caatttggcg ccgttgccaa ttgggtgttt gtttgttaca tttgagattt cagacttgct 120

tagatcaagt tctttttcaa ttttcttttt 150

<210> 37
<211> 11
<212> DNA
<213> Glycine max

<400> 37
tggcgccgtt g 11

<210> 38
<211> 15
<212> DNA
<213> Glycine max

<400> 38
tggcgccgtt gccgg 15

<210> 39
<211> 27
<212> DNA
<213> Glycine max

<400> 39
tttttggcgc cgttgtcggg gattttg 27

<210> 40
<211> 9
<212> DNA
<213> Glycine max

<400> 40
tttgggggga 9

<210> 41
<211> 16
<212> DNA
<213> Glycine max

<400> 41
tttaatttgg gggatt 16

<210> 42
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 42
gggatccgca attagaatct 20

<210> 43
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 43
cgaattcggt ccacttcgga 20

<210> 44
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 44
ccacaagatt ctaattgcgg attc 24

<210> 45
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 45
ccgaaatgga ccgaacccga catc 24

<210> 46
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 46
tttccaggct cttgacgaga tttg 24

<210> 47
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 47
cgactcgagc tccatagcga tg 22

<210> 48
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> primer

<400> 48
cggattgggc cgaaatggac cgaa 24

<210> 49
<211> 18
<212> DNA
<213> Arabidopsis thaliana

<400> 49
gaggacttgg ggggcaaa 18

<210> 50
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary motif

<221> VARIANT
<222> 2-3, 5-7, 9-12
<223> Xaa = Any Amino Acid

<400> 50
Cys Xaa Xaa Cys Xaa Xaa Xaa His Xaa Xaa Xaa Xaa Cys
1 5 10

<210> 51
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary motif

<400> 51
Leu Ile Asp Leu Gly Ala
1 5

<210> 52
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<400> 52
Lys Thr Ala Phe
1

<210> 53
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<221> VARIANT
<222> 2
<223> Xaa = Pro or Ser

<400> 53
Met Xaa Phe Gly Leu Cys Asn Ala
 1   5

<210> 54
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<221> VARIANT
<222> 1
<223> Xaa = Val, Ile, or Met

<221> VARIANT
<222> 9
<223> Xaa = Ser or Trp

<221> VARIANT
<222> 10
<223> Xaa = Val or Ile

<400> 54
Xaa Glu Val Phe Met Asp Asp Phe Xaa Xaa
 1   5   10

<210> 55
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<221> VARIANT
<222> 12
<223> Xaa = Ile or Val

<400> 55
Phe Glu Leu Met Cys Asp Ala Ser Asp Tyr Ala Xaa Gly Ala Val Leu
 1   5   10   15
Gly Gln Arg

<210> 56
<211> 27
<212> PRT

<213> Artificial Sequence

<220>
<223> consensus sequence

<221> VARIANT
<222> 4
<223> Xaa = Thr or Ile

<221> VARIANT
<222> 8
<223> Xaa = Leu or Met

<221> VARIANT
<222> 13
<223> Xaa = Phe or Tyr

<221> VARIANT
<222> 15
<223> Xaa = Leu or Phe

<221> VARIANT
<222> 19
<223> Xaa = Arg or Lys

<221> VARIANT
<222> 23
<223> Xaa = Ile or Val

<221> VARIANT
<222> 26
<223> Xaa = Arg or Lys

<400> 56
Tyr Ala Thr Xaa Glu Lys Glu Xaa Leu Ala Ile Val Xaa Ala Xaa Glu
 1   5   10   15
Lys Phe Xaa Ser Tyr Leu Xaa Gly Ser Xaa Val
            20   25

<210> 57
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<221> VARIANT
<222> 4, 6-7, 11-40, 43
<223> Xaa = Any Amino Acid

<400> 57
His Cys His Xaa Ser Xaa Xaa Gly Gly His Xaa Xaa Xaa Xaa Xaa Xaa
 1   5   10   15
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20   25   30
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Asp Xaa Cys Gln Arg

35 40 45

<210> 58
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<221> VARIANT
<222> 6
<223> Xaa = Ile, Val, or Met

<400> 58
Trp Gly Ile Asp Phe Xaa Gly Pro
1 5

<210> 59
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<221> VARIANT
<222> 7
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> 10
<223> Xaa = Ala or Val

<400> 59
Pro Tyr His Pro Gln Thr Xaa Gly Gln Xaa Glu
1 5 10

<210> 60
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> consensus sequence

<221> misc_feature
<222> 11, 12
<223> n = A,T,C or G

<400> 60
atttggggra nnt 13

<210> 61
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<221> VARIANT
<222> 5, 8
<223> Xaa = Arg or Lys

<400> 61
Gln Met Ala Ser Xaa Lys Arg Xaa Ala
 1   5

<210> 62
<211> 6
<212> PRT
<213> Pisum sativum

<400> 62
Ala Ser Lys Lys Arg Lys
 1   5